

TITLE OF THE INVENTION

PROTEIN-PROTEIN INTERACTIONS

CROSS-REFERENCE TO RELATED APPLICATIONS

5 [0001] The present application is related to U.S. provisional patent application Serial No. 60/259,572, filed on 4 January 2001, incorporated herein by reference, and claims priority thereto under 35 USC §119(e).

BACKGROUND OF THE INVENTION

10 [0002] The present invention relates to the discovery of novel protein-protein interactions that are involved in mammalian physiological pathways, including physiological disorders or diseases. Examples of physiological disorders and diseases include non-insulin dependent diabetes mellitus (NIDDM), neurodegenerative disorders, such as Alzheimer's Disease (AD), and the like.

15 Thus, the present invention is directed to complexes of these proteins and/or their fragments, antibodies to the complexes, diagnosis of physiological generative disorders (including diagnosis of a predisposition to and diagnosis of the existence of the disorder), drug screening for agents which modulate the interaction of proteins described herein, and identification of additional proteins in the pathway common to the proteins described herein.

20 [0003] The publications and other materials used herein to illuminate the background of the invention, and in particular, cases to provide additional details respecting the practice, are incorporated herein by reference, and for convenience, are referenced by author and date in the following text and respectively grouped in the appended Bibliography.

25 [0004] Many processes in biology, including transcription, translation and metabolic or signal transduction pathways, are mediated by non-covalently associated protein complexes. The formation of protein-protein complexes or protein-DNA complexes produce the most efficient chemical machinery. Much of modern biological research is concerned with identifying proteins involved in cellular processes, determining their functions, and how, when and where they interact with other proteins involved in specific pathways. Further, with rapid advances in genome sequencing, there is a need to define protein linkage maps, i.e., detailed inventories of protein
30 interactions that make up functional assemblies of proteins or protein complexes or that make up physiological pathways.

[0005] Recent advances in human genomics research has led to rapid progress in the identification of novel genes. In applications to biological and pharmaceutical research, there is a

need to determine functions of gene products. A first step in defining the function of a novel gene is to determine its interactions with other gene products in appropriate context. That is, since proteins make specific interactions with other proteins or other biopolymers as part of functional assemblies or physiological pathways, an appropriate way to examine function of a gene is to determine its physical relationship with other genes. Several systems exist for identifying protein interactions and hence relationships between genes.

[0006] There continues to be a need in the art for the discovery of additional protein-protein interactions involved in mammalian physiological pathways. There continues to be a need in the art also to identify the protein-protein interactions that are involved in mammalian physiological disorders and diseases, and to thus identify drug targets.

SUMMARY OF THE INVENTION

[0007] The present invention relates to the discovery of protein-protein interactions that are involved in mammalian physiological pathways, including physiological disorders or diseases, and to the use of this discovery. The identification of the interacting proteins described herein provide new targets for the identification of useful pharmaceuticals, new targets for diagnostic tools in the identification of individuals at risk, sequences for production of transformed cell lines, cellular models and animal models, and new bases for therapeutic intervention in such physiological pathways

[0008] Thus, one aspect of the present invention is protein complexes. The protein complexes are a complex of (a) two interacting proteins, (b) a first interacting protein and a fragment of a second interacting protein, (c) a fragment of a first interacting protein and a second interacting protein, or (d) a fragment of a first interacting protein and a fragment of a second interacting protein. The fragments of the interacting proteins include those parts of the proteins, which interact to form a complex. This aspect of the invention includes the detection of protein interactions and the production of proteins by recombinant techniques. The latter embodiment also includes cloned sequences, vectors, transfected or transformed host cells and transgenic animals.

[0009] A second aspect of the present invention is an antibody that is immunoreactive with the above complex. The antibody may be a polyclonal antibody or a monoclonal antibody. While the antibody is immunoreactive with the complex, it is not immunoreactive with the component parts of the complex. That is, the antibody is not immunoreactive with a first interactive protein, a fragment of a first interacting protein, a second interacting protein or a fragment of a second

interacting protein. Such antibodies can be used to detect the presence or absence of the protein complexes.

[0010] A third aspect of the present invention is a method for diagnosing a predisposition for physiological disorders or diseases in a human or other animal. The diagnosis of such disorders includes a diagnosis of a predisposition to the disorders and a diagnosis for the existence of the disorders. In accordance with this method, the ability of a first interacting protein or fragment thereof to form a complex with a second interacting protein or a fragment thereof is assayed, or the genes encoding interacting proteins are screened for mutations in interacting portions of the protein molecules. The inability of a first interacting protein or fragment thereof to form a complex, or the presence of mutations in a gene within the interacting domain, is indicative of a predisposition to, or existence of a disorder. In accordance with one embodiment of the invention, the ability to form a complex is assayed in a two-hybrid assay. In a first aspect of this embodiment, the ability to form a complex is assayed by a yeast two-hybrid assay. In a second aspect, the ability to form a complex is assayed by a mammalian two-hybrid assay. In a second embodiment, the ability to form a complex is assayed by measuring *in vitro* a complex formed by combining said first protein and said second protein. In one aspect the proteins are isolated from a human or other animal. In a third embodiment, the ability to form a complex is assayed by measuring the binding of an antibody, which is specific for the complex. In a fourth embodiment, the ability to form a complex is assayed by measuring the binding of an antibody that is specific for the complex with a tissue extract from a human or other animal. In a fifth embodiment, coding sequences of the interacting proteins described herein are screened for mutations.

[0011] A fourth aspect of the present invention is a method for screening for drug candidates which are capable of modulating the interaction of a first interacting protein and a second interacting protein. In this method, the amount of the complex formed in the presence of a drug is compared with the amount of the complex formed in the absence of the drug. If the amount of complex formed in the presence of the drug is greater than or less than the amount of complex formed in the absence of the drug, the drug is a candidate for modulating the interaction of the first and second interacting proteins. The drug promotes the interaction if the complex formed in the presence of the drug is greater and inhibits (or disrupts) the interaction if the complex formed in the presence of the drug is less. The drug may affect the interaction directly, i.e., by modulating the binding of the two proteins, or indirectly, e.g., by modulating the expression of one or both of the proteins.

[0012] A fifth aspect of the present invention is a model for such physiological pathways, disorders or diseases. The model may be a cellular model or an animal model, as further described herein. In accordance with one embodiment of the invention, an animal model is prepared by creating transgenic or "knock-out" animals. The knock-out may be a total knock-out, i.e., the desired gene is deleted, or a conditional knock-out, i.e., the gene is active until it is knocked out at a determined time. In a second embodiment, a cell line is derived from such animals for use as a model. In a third embodiment, an animal model is prepared in which the biological activity of a protein complex of the present invention has been altered. In one aspect, the biological activity is altered by disrupting the formation of the protein complex, such as by the binding of an antibody or small molecule to one of the proteins which prevents the formation of the protein complex. In a second aspect, the biological activity of a protein complex is altered by disrupting the action of the complex, such as by the binding of an antibody or small molecule to the protein complex which interferes with the action of the protein complex as described herein. In a fourth embodiment, a cell model is prepared by altering the genome of the cells in a cell line. In one aspect, the genome of the cells is modified to produce at least one protein complex described herein. In a second aspect, the genome of the cells is modified to eliminate at least one protein of the protein complexes described herein.

[0013] A sixth aspect of the present invention are nucleic acids coding for novel proteins discovered in accordance with the present invention and the corresponding proteins and antibodies.

[0014] A seventh aspect of the present invention is a method of screening for drug candidates useful for treating a physiological disorder. In this embodiment, drugs are screened on the basis of the association of a protein with a particular physiological disorder. This association is established in accordance with the present invention by identifying a relationship of the protein with a particular physiological disorder. The drugs are screened by comparing the activity of the protein in the presence and absence of the drug. If a difference in activity is found, then the drug is a drug candidate for the physiological disorder. The activity of the protein can be assayed *in vitro* or *in vivo* using conventional techniques, including transgenic animals and cell lines of the present invention.

DETAILED DESCRIPTION OF THE INVENTION

[0015] The present invention is the discovery of novel interactions between proteins described herein. The genes coding for some of these proteins may have been cloned previously,

but their potential interaction in a physiological pathway or with a particular protein was unknown.

Alternatively, the genes coding for some of these proteins have not been cloned previously and represent novel genes. These proteins are identified using the yeast two-hybrid method and searching a human total brain library, as more fully described below.

5 [0016] According to the present invention, new protein-protein interactions have been discovered. The discovery of these interactions has identified several protein complexes for each protein-protein interaction. The protein complexes for these interactions are set forth below in Tables 1-12, which also identifies the new protein-protein interactions of the present invention.

TABLE 1

Protein Complexes IKKb/LDHM Interaction

IkappaB kinase beta (IKKb) and lactate dehydrogenase A (LDHM)

A fragment of IKKb and LDHM

IKKb and a fragment of LDHM

A fragment of IKKb and a fragment of LDHM

TABLE 2

Protein Complexes IKKb/EIF3S10 Interaction

IkappaB kinase beta (IKKb) and translation initiation factor 3 (EIF3S10)

A fragment of IKKb and EIF3S10

IKKb and a fragment of EIF3S10

A fragment of IKKb and a fragment of EIF3S10

TABLE 3

Protein Complexes IKKb/SLAP2 Interaction

IkappaB kinase beta (IKKb) and sarcolemmal associated protein-2 (SLAP2)

A fragment of IKKb and SLAP2

IKKb and a fragment of SLAP2

A fragment of IKKb and a fragment of SLAP2

TABLE 4

Protein Complexes IKKb/KIAA0614 Interaction

IkappaB kinase beta (IKKb) and KIAA0614
 A fragment of IKKb and KIAA0614
 5 IKKb and a fragment of KIAA0614
 A fragment of IKKb and a fragment of KIAA0614

TABLE 5

Protein Complexes IKKb/SART-1 Interaction

IkappaB kinase beta (IKKb) and SART-1
 A fragment of IKKb and SART-1
 IKKb and a fragment of SART-1
 A fragment of IKKb and a fragment of SART-1

TABLE 6

Protein Complexes IKKb/GBDR1 Interaction

IkappaB kinase beta (IKKb) and glioblastoma differentiation-related protein (GBDR1)
 A fragment of IKKb and GBDR1
 IKKb and a fragment of GBDR1
 20 A fragment of IKKb and a fragment of GBDR1

TABLE 7

Protein Complexes IKKa/GBDR1 Interaction

IkappaB kinase alpha (IKKa) and glioblastoma differentiation-related protein (GBDR1)
 25 A fragment of IKKa and GBDR1
 IKKa and a fragment of GBDR1
 A fragment of IKKa and a fragment of GBDR1

TABLE 8

Protein Complexes IKKg/I-TRAF Interaction

IkappaB kinase gamma (IKKg) and TRAF-interacting protein (I-TRAF)

A fragment of IKKg and I-TRAF

5 IKKg and a fragment of I-TRAF

A fragment of IKKg and a fragment of I-TRAF

TABLE 9

Protein Complexes IKK-i/I-TRAF Interaction

IkappaB kinase, inducible (IKK-i) and TRAF-interacting protein (I-TRAF)

A fragment of IKK-i and I-TRAF

IKK-i and a fragment of I-TRAF

A fragment of IKK-i and a fragment of I-TRAF

TABLE 10

Protein Complexes IKK-i/NUMA1 Interaction

IkappaB kinase, inducible (IKK-i) and nuclear mitotic apparatus protein 1 (NUMA1)

A fragment of IKK-i and NUMA1

IKK-i and a fragment of NUMA1

20 A fragment of IKK-i and a fragment of NUMA1

TABLE 11

Protein Complexes IKK-i/SPA-1 Interaction

IkappaB kinase, inducible (IKK-i) and signal-induced proliferation associated protein (SPA1)

25 A fragment of IKK-i and SPA1

IKK-i and a fragment of SPA1

A fragment of IKK-i and a fragment of SPA1

TABLE 12

Protein Complexes IKK-i/PN13730 Interaction

IkappaB kinase, inducible (IKK-i) and novel protein PN13730

A fragment of IKK-i and PN13730

5 IKK-i and a fragment of PN13730

A fragment of IKK-i and a fragment of PN13730

[0017] The involvement of above interactions in particular pathways is as follows.

[0018] Many cellular proteins exert their function by interacting with other proteins in the cell. Examples of this are found in the formation of multiprotein complexes and the association of enzymes with their substrates. It is widely believed that a great deal of information can be gained by understanding individual protein-protein interactions, and that this is useful in identifying complex networks of interacting proteins that participate in the workings of normal cellular functions. Ultimately, the knowledge gained by characterizing these networks can lead to valuable insight into the causes of human diseases and can eventually lead to the development of therapeutic strategies. The yeast two-hybrid assay is a powerful tool for determining protein-protein interactions and it has been successfully used for studying human disease pathways. In one variation of this technique, a protein of interest (or a portion of that protein) is expressed in a population of yeast cells that collectively contain all protein sequences. Yeast cells that possess protein sequences that interact with the protein of interest are then genetically selected, and the identity of those interacting proteins are determined by DNA sequencing. Thus, proteins that can be demonstrated to interact with a protein known to be involved in a human disease are therefore also implicated in that disease. Proteins identified in the first round of two-hybrid screening can be subsequently used in a second round of two-hybrid screening, allowing the identification of multiple proteins in the complex network of interactions in a disease pathway.

[0019] Nuclear factor kappaB (NFkB) is an inducible transcription factor that regulates a large number of genes, particularly those involved in the inflammatory and immune responses (Barnes and Karin, 1997; Baeuerle and Baichwal, 1997). NFkB has been demonstrated to be inappropriately regulated in a number of human inflammatory disorders, including rheumatoid and osteoarthritis, asthma, arteriosclerosis and inflammatory bowel disease, as well as some cancers (Luque and Gelinas, 1997; Foxwell et al., 1998; Barnes and Adcock, 1998; Neurath et al., 1998; Hatada et al., 2000). Inhibiting NFkB activation has many potential applications in treating these

diseases, and consequently is an area of intense interest for drug development. One mechanism by which steroids exert their broad-spectrum anti-inflammatory action is by inhibiting the activation of NFkB. By identifying non-steroidal means of inhibiting NFkB activation, it is hoped a class of novel immunosuppressive drugs that has the potency of steroids without their toxicity can be developed.

[0020] NFkB activity is controlled by protein-protein interactions that alter its subcellular localization (Karin and Ben-Neriah, 2000; Karin, 1999; Mercurio and Manning, 1999). In unstimulated cells, NFkB is inactive and sequestered in the cytoplasm due to its interaction with IkappaB (IkB), which masks the NFkB nuclear localization signal. Upon stimulation, IkB is phosphorylated, which targets it for ubiquitination and proteasome-mediated degradation. Disruption of the IkB/NFkB complex frees NFkB to enter the nucleus and activate transcription of proinflammatory genes. A key step in NFkB activation is the initial phosphorylation of IkB; this is accomplished by IkB-kinase (IKK) family members, which are in turn responsive to signals from cell surface receptors for factors such as TNF-alpha and IL-1. Clearly, identifying all of the proteins involved in NFkB activation is necessary to understand the process by which extracellular signals are transduced into NFkB-mediated transcriptional responses. Furthermore, identification of these proteins will increase the repertoire of potential targets for therapeutic intervention in the treatment of diseases due to defects involving NFkB activation, such as arthritis, asthma, and cancer.

[0021] IkB kinases (IKKs) are responsible for signal-induced phosphorylation IkB, leading to IkB degradation and activation of NFkB. These proteins appear to function as a complex of IKK family members, and may interact with other cellular factors as well. Consequently, the IKKs and proteins with which they interact are potential targets of anti-inflammatory (and other) drugs. Four IKKs [IKK-alpha (IKKa), IKK-beta (IKKb), IKK-gamma (IKKg), and inducible IKK (IKK-i)] have been identified (reviewed in Karin and Ben-Neriah, 2000; Karin, 1999; Mercurio and Manning, 19998-10). These proteins were used in yeast two-hybrid assays to identify IKK-interacting proteins.

[0022] Six new interactions were identified for IKK-beta (IKKb). The first is with the squamous cell carcinoma antigen SART-1. SART-1 was identified as an antigen on human squamous cell carcinoma cells that is recognized by cytotoxic T-lymphocytes. SART-1 does not have any recognizable structural domains that might give clues to its function. Interestingly, SART-1 has a high degree of homology to the mouse Haf protein (GenBank accession AF129931). Haf is described as a hypoxia associated factor that induces the expression of erythropoietin and VEGF.

This similarity and the interaction with IKKb suggest SART-1 is involved in intracellular signaling both in response to, and leading to the production of, cell signaling factors.

[0023] The second IKKb interactor is a subunit of translation initiation factor 3 (EIF3S10). EIF3S10 is the largest subunit of the EIF3 complex. It contains a so-called PCI domain that is found in other proteins also found in large complexes, such as components of the COP9 signalosome (Scholler et al., 1997). The interaction of EIF3S20 with IKKb suggests that phosphorylation of the translation machinery may be part of the inflammatory response. This possibility is further supported by our identification of interactions between MAPKAP-K3, a protein kinase involved in the inflammatory response, and the translation-associated proteins ERF-2, SUI1, and PAIP1.

[0024] The next IKKb interactor is the lactate dehydrogenase M chain (also known as LDH-A) was found to be an interactor. LDH is the last enzyme involved in anaerobic glycolysis, and resides in the cytosol. Although the significance of this interaction is not entirely clear, the demonstrated interaction with IKKb suggests that LDH can act as a phosphorylation substrate of IKKb, and further suggests a link between NFkB activation and cellular metabolism.

[0025] IKKb is shown to interact with the sarcolemmal-associated protein SLAP-2. The SLAP proteins are a family of amphipathic alpha-helical proteins that associate with the membrane and form coiled-coil structures (Wigle et al., 1997). We have previously identified an interaction between SLAP-2 and the insulin-regulated aminopeptidase IRAP, suggesting this protein functions both in insulin-dependent and inflammation-related signaling pathways.

[0026] We have identified an interaction between IKKb and the hypothetical protein KIAA0614. The function of KIAA0614 is largely unknown, however there does appear to be a putative HECT domain in the KIAA0614 protein sequence. The HECT domain is the consensus sequence found in ubiquitin transferases or so-called E3 ubiquitin ligases. IKKb contains a ubiquitin-like region that may be responsible for this interaction. In addition, KIAA0614 closely related to a protein described in the public databases as a protein phosphatase (GenBank accession AF174498). This suggests that KIAA0614 and IKKb may act together to control the phosphorylation status of cellular substrates such as Ikb.

[0027] The next interactor, the glioblastoma cell differentiation-related protein GBDR1, was found in yeast two-hybrid searches using both IKK-alpha and IKK-beta. The function of GBDR1 is not known but sequence analysis indicates the presence of two ubiquitin-associated domains. Consistent with this, the IKK-beta used to isolate GBDR1 contains a ubiquitin-like domain. In

contrast, the fragment of IKK-alpha that associates with GBDR1 includes a helix-loop-helix domain rather than the ubiquitin-like domain. Nonetheless, the interaction of the same domain of GBDR1 with two different IKKs strongly suggests this protein is part of the signal transduction cascade that leads to NFkB activation.

[0028] One interactor for IKK-gamma (IKKg, also known as NEMO) was identified. This protein, I-TRAF, is a known component of the NFkB activation cascade. I-TRAF is known to bind to the conserved C-terminal domain of TRAF proteins and inhibit TRAF-mediated NF-kappa-B activation (Ling and Goeddel, 2000). Phosphorylation of I-TRAF results in its dissociation from TRAF and the subsequent activation of NFkB. We and others have found that another IKK (IKK-i) is able to interact with, and phosphorylate, I-TRAF (Nomura et al., 2000). The interaction with IKK-gamma may similarly result in modification of I-TRAF. However, such a role for IKKg is likely indirect, since IKKg appears to be a non-catalytic IKK family member. This notion is consistent with the fact that the domain of IKK-i with which I-TRAF interacts is a C-terminal (non-kinase) region of the protein.

[0029] The inducible Ikb kinase (IKK-i) was found to interact with three proteins. The first of these is the signal-induced proliferation associated protein SPA1. SPA-1 is over 90% identical to the murine homolog, which was originally isolated based on its inducible expression in lymphoid cells stimulated with IL-2; it was further shown that murine SPA1 hampers mitogen-induced cell cycle progression when abnormally or prematurely expressed (Hattori et al., 1995). The N-terminal domains of both the human and murine SPA1 proteins are highly homologous to the human Rap1 GTPase-activating protein (GAP). Human SPA1 exhibits GAP activity for Rap1 and Rap2, but not for Ras, Rho, or Ran (Kurachi et al., 1997). In addition to the N-terminal GTPase activating domain, human SPA1 contains predicted coiled-coil, PDZ, and transmembrane domains. Human SPA1 is localized primarily to the perinuclear region and is widely expressed, with highest expression levels in lymphoid organs. The interaction with IKK-i suggests SPA-1 is involved in NFkB activation.

[0030] IKK-i is also found to interact with the nuclear mitotic apparatus protein NUMA1. NUMA1 is found in the nucleus during interphase and is associated with isolated nuclear matrices, and specifically localizes to the spindle apparatus during mitosis in a manner that suggests it is involved in the early steps of nuclear reassembly (Lydersen and Pettijohn, 1980). Analysis of the 2101 amino acid NUMA1 protein reveals an unusually long central coiled-coil domain (>1400 amino acids). Interestingly, NUMA1 is one of a handful of proteins to which RAR-alpha can be fused in acute promyelocytic leukemia (APL). The most prevalent RAR-alpha fusion partner in

APL is PML, and it has been proposed that disruption of PML organization is responsible for the APL phenotype. In rare cases of APL, the ligand- and DNA-binding domains of RAR-alpha are fused to the 5' exons of NUMA1, resulting in a fusion protein that exists in sheet-like nuclear aggregates (Wells et al., 1997). Wells et al. further demonstrate that PML organization is normal in cells expressing the RAR-alpha/NUMA1 fusion, suggesting that interference with retinoid signaling, and not disruption of PML organization, is essential to the APL phenotype and implicating an element of the mitotic apparatus in the molecular pathogenesis of human malignancy. The interaction of NUMA1 with an IKK suggests that cellular processes, such as mitosis and nuclear assembly, are under control of the same signaling pathways that activate NFkB. In support of this, we have previously found interactions between NUMA1 and the signaling proteins MAPKAP-K3, PRAK, AKT1, and AKT2.

[0031] The final interaction for IKK-i is with the novel protein PN13730. PN13730 is a protein fragment 494 amino acids in length that contains predicted coiled-coil domains, a spectrin repeat, and regions similar to the leukemia inhibiting factor/oncostatin-M small cytokine signature and the syntaxin N-terminal motif. The prey construct isolated by ProNet encodes amino acids 203-493 of PN13730. EST analysis suggests that PN13730 is expressed in a number of tissues including breast, skin and ovary. Subsequent to the identification of PN13730, the full length sequence of this protein has been identified and, along with the cDNA sequence, is set forth in GenBank accession number AJ292348. PN13730 corresponds to the N-terminus of AJ292348.

[0032] The proteins disclosed in the present invention were found to interact with their corresponding proteins in the yeast two-hybrid system. Because of the involvement of the corresponding proteins in the physiological pathways disclosed herein, the proteins disclosed herein also participate in the same physiological pathways. Therefore, the present invention provides a list of uses of these proteins and DNA encoding these proteins for the development of diagnostic and therapeutic tools useful in the physiological pathways. This list includes, but is not limited to, the following examples.

Two-Hybrid System

[0033] The principles and methods of the yeast two-hybrid system have been described in detail elsewhere (e.g., Bartel and Fields, 1997; Bartel et al., 1993; Fields and Song, 1989; Chevray and Nathans, 1992). The following is a description of the use of this system to identify proteins that interact with a protein of interest.

[0034] The target protein is expressed in yeast as a fusion to the DNA-binding domain of the yeast Gal4p. DNA encoding the target protein or a fragment of this protein is amplified from cDNA by PCR or prepared from an available clone. The resulting DNA fragment is cloned by ligation or recombination into a DNA-binding domain vector (e.g., pGBT9, pGBT.C, pAS2-1) such that an in-frame fusion between the Gal4p and target protein sequences is created.

[0035] The target gene construct is introduced, by transformation, into a haploid yeast strain. A library of activation domain fusions (i.e., adult brain cDNA cloned into an activation domain vector) is introduced by transformation into a haploid yeast strain of the opposite mating type. The yeast strain that carries the activation domain constructs contains one or more Gal4p-responsive reporter gene(s), whose expression can be monitored. Examples of some yeast reporter strains include Y190, PJ69, and CBY14a. An aliquot of yeast carrying the target gene construct is combined with an aliquot of yeast carrying the activation domain library. The two yeast strains mate to form diploid yeast and are plated on media that selects for expression of one or more Gal4p-responsive reporter genes. Colonies that arise after incubation are selected for further characterization.

[0036] The activation domain plasmid is isolated from each colony obtained in the two-hybrid search. The sequence of the insert in this construct is obtained by the dideoxy nucleotide chain termination method. Sequence information is used to identify the gene/protein encoded by the activation domain insert via analysis of the public nucleotide and protein databases. Interaction of the activation domain fusion with the target protein is confirmed by testing for the specificity of the interaction. The activation domain construct is co-transformed into a yeast reporter strain with either the original target protein construct or a variety of other DNA-binding domain constructs. Expression of the reporter genes in the presence of the target protein but not with other test proteins indicates that the interaction is genuine.

[0037] In addition to the yeast two-hybrid system, other genetic methodologies are available for the discovery or detection of protein-protein interactions. For example, a mammalian two-hybrid system is available commercially (Clontech, Inc.) that operates on the same principle as the yeast two-hybrid system. Instead of transforming a yeast reporter strain, plasmids encoding DNA-binding and activation domain fusions are transfected along with an appropriate reporter gene (e.g., *lacZ*) into a mammalian tissue culture cell line. Because transcription factors such as the *Saccharomyces cerevisiae* Gal4p are functional in a variety of different eukaryotic cell types, it would be expected that a two-hybrid assay could be performed in virtually any cell line of eukaryotic origin (e.g., insect

cells (SF9), fungal cells, worm cells, etc.). Other genetic systems for the detection of protein-protein interactions include the so-called SOS recruitment system (Aronheim et al., 1997).

Protein-protein interactions

[0038] Protein interactions are detected in various systems including the yeast two-hybrid system, affinity chromatography, co-immunoprecipitation, subcellular fractionation and isolation of large molecular complexes. Each of these methods is well characterized and can be readily performed by one skilled in the art. See, e.g., U.S. Patents No. 5,622,852 and 5,773,218, and PCT published applications No. WO 97/27296 and WO 99/65939, each of which are incorporated herein by reference.

[0039] The protein of interest can be produced in eukaryotic or prokaryotic systems. A cDNA encoding the desired protein is introduced in an appropriate expression vector and transfected in a host cell (which could be bacteria, yeast cells, insect cells, or mammalian cells). Purification of the expressed protein is achieved by conventional biochemical and immunochemical methods well known to those skilled in the art. The purified protein is then used for affinity chromatography studies: it is immobilized on a matrix and loaded on a column. Extracts from cultured cells or homogenized tissue samples are then loaded on the column in appropriate buffer, and non-binding proteins are eluted. After extensive washing, binding proteins or protein complexes are eluted using various methods such as a gradient of pH or a gradient of salt concentration. Eluted proteins can then be separated by two-dimensional gel electrophoresis, eluted from the gel, and identified by micro-sequencing. The purified proteins can also be used for affinity chromatography to purify interacting proteins disclosed herein. All of these methods are well known to those skilled in the art.

[0040] Similarly, both proteins of the complex of interest (or interacting domains thereof) can be produced in eukaryotic or prokaryotic systems. The proteins (or interacting domains) can be under control of separate promoters or can be produced as a fusion protein. The fusion protein may include a peptide linker between the proteins (or interacting domains) which, in one embodiment, serves to promote the interaction of the proteins (or interacting domains). All of these methods are also well known to those skilled in the art.

[0041] Purified proteins of interest, individually or a complex, can also be used to generate antibodies in rabbit, mouse, rat, chicken, goat, sheep, pig, guinea pig, bovine, and horse. The methods used for antibody generation and characterization are well known to those skilled in the

art. Monoclonal antibodies are also generated by conventional techniques. Single chain antibodies are further produced by conventional techniques.

[0042] DNA molecules encoding proteins of interest can be inserted in the appropriate expression vector and used for transfection of eukaryotic cells such as bacteria, yeast, insect cells, or mammalian cells, following methods well known to those skilled in the art. Transfected cells expressing both proteins of interest are then lysed in appropriate conditions, one of the two proteins is immunoprecipitated using a specific antibody, and analyzed by polyacrylamide gel electrophoresis. The presence of the binding protein (co-immunoprecipitated) is detected by immunoblotting using an antibody directed against the other protein. Co-immunoprecipitation is a method well known to those skilled in the art.

[0043] Transfected eukaryotic cells or biological tissue samples can be homogenized and fractionated in appropriate conditions that will separate the different cellular components. Typically, cell lysates are run on sucrose gradients, or other materials that will separate cellular components based on size and density. Subcellular fractions are analyzed for the presence of proteins of interest with appropriate antibodies, using immunoblotting or immunoprecipitation methods. These methods are all well known to those skilled in the art.

Disruption of protein-protein interactions

[0044] It is conceivable that agents that disrupt protein-protein interactions can be beneficial in many physiological disorders, including, but not-limited to NIDDM, AD and others disclosed herein. Each of the methods described above for the detection of a positive protein-protein interaction can also be used to identify drugs that will disrupt said interaction. As an example, cells transfected with DNAs coding for proteins of interest can be treated with various drugs, and co-immunoprecipitations can be performed. Alternatively, a derivative of the yeast two-hybrid system, called the reverse yeast two-hybrid system (Leanna and Hannink, 1996), can be used, provided that the two proteins interact in the straight yeast two-hybrid system.

Modulation of protein-protein interactions

[0045] Since the interactions described herein are involved in a physiological pathway, the identification of agents which are capable of modulating the interactions will provide agents which can be used to track physiological disorder or to use lead compounds for development of therapeutic agents. An agent may modulate expression of the genes of interacting proteins, thus affecting

interaction of the proteins. Alternatively, the agent may modulate the interaction of the proteins.

The agent may modulate the interaction of wild-type with wild-type proteins, wild-type with mutant proteins, or mutant with mutant proteins. Agents which may be used to modulate the protein interaction include a peptide, an antibody, a nucleic acid, an antisense compound or a ribozyme.

5 The nucleic acid may encode the antibody or the antisense compound. The peptide may be at least 4 amino acids of the sequence of either of the interacting proteins. Alternatively, the peptide may be from 4 to 30 amino acids (or from 8 to 20 amino acids) that is at least 75% identical to a contiguous span of amino acids of either of the interacting proteins. The peptide may be covalently linked to a transporter capable of increasing cellular uptake of the peptide. Examples of a suitable transporter include penetratins, *l*-Tat₄₉₋₅₇, *d*-Tat₄₉₋₅₇, retro-inverso isomers of *l*- or *d*-Tat₄₉₋₅₇, L-arginine oligomers, D-arginine oligomers, L-lysine oligomers, D-lysine oligomers, L-histidine oligomers, D-histidine oligomers, L-ornithine oligomers, D-ornithine oligomers, short peptide sequences derived from fibroblast growth factor, Galparan, and HSV-1 structural protein VP22, and peptoid analogs thereof. Agents can be tested using transfected host cells, cell lines, cell models or animals, such as described herein, by techniques well known to those of ordinary skill in the art, such as disclosed in U.S. Patents Nos. 5,622,852 and 5,773,218, and PCT published application Nos. WO 97/27296 and WO 99/65939, each of which are incorporated herein by reference. The modulating effect of the agent can be tested *in vivo* or *in vitro*. Agents can be provided for testing in a phage display library or a combinatorial library. Exemplary of a method to screen agents is to measure the effect that the agent has on the formation of the protein complex.

Mutation screening

[0046] The proteins disclosed in the present invention interact with one or more proteins known to be involved in a physiological pathway, such as in NIDDM, AD or pathways described herein. Mutations in interacting proteins could also be involved in the development of the physiological disorder, such as NIDDM, AD or disorders described herein, for example, through a modification of protein-protein interaction, or a modification of enzymatic activity, modification of receptor activity, or through an unknown mechanism. Therefore, mutations can be found by sequencing the genes for the proteins of interest in patients having the physiological disorder, such as insulin, and non-affected controls. A mutation in these genes, especially in that portion of the gene involved in protein interactions in the physiological pathway, can be used as a diagnostic tool and the mechanistic understanding the mutation provides can help develop a therapeutic tool.

Screening for at-risk individuals

[0047] Individuals can be screened to identify those at risk by screening for mutations in the protein disclosed herein and identified as described above. Alternatively, individuals can be screened by analyzing the ability of the proteins of said individual disclosed herein to form natural complexes. Further, individuals can be screened by analyzing the levels of the complexes or individual proteins of the complexes or the mRNA encoding the protein members of the complexes. Techniques to detect the formation of complexes, including those described above, are known to those skilled in the art. Techniques and methods to detect mutations are well known to those skilled in the art. Techniques to detect the level of the complexes, proteins or mRNA are well known to those skilled in the art.

Cellular models of Physiological Disorders

[0048] A number of cellular models of many physiological disorders or diseases have been generated. The presence and the use of these models are familiar to those skilled in the art. As an example, primary cell cultures or established cell lines can be transfected with expression vectors encoding the proteins of interest, either wild-type proteins or mutant proteins. The effect of the proteins disclosed herein on parameters relevant to their particular physiological disorder or disease can be readily measured. Furthermore, these cellular systems can be used to screen drugs that will influence those parameters, and thus be potential therapeutic tools for the particular physiological disorder or disease. Alternatively, instead of transfecting the DNA encoding the protein of interest, the purified protein of interest can be added to the culture medium of the cells under examination, and the relevant parameters measured.

Animal models

[0049] The DNA encoding the protein of interest can be used to create animals that overexpress said protein, with wild-type or mutant sequences (such animals are referred to as "transgenic"), or animals which do not express the native gene but express the gene of a second animal (referred to as "transplacement"), or animals that do not express said protein (referred to as "knock-out"). The knock-out animal may be an animal in which the gene is knocked out at a determined time. The generation of transgenic, transplacement and knock-out animals (normal and conditioned) uses methods well known to those skilled in the art.

[0050] In these animals, parameters relevant to the particular physiological disorder can be measured. These parameters may include receptor function, protein secretion *in vivo* or *in vitro*, survival rate of cultured cells, concentration of particular protein in tissue homogenates, signal transduction, behavioral analysis, protein synthesis, cell cycle regulation, transport of compounds across cell or nuclear membranes, enzyme activity, oxidative stress, production of pathological products, and the like. The measurements of biochemical and pathological parameters, and of behavioral parameters, where appropriate, are performed using methods well known to those skilled in the art. These transgenic, transplacement and knock-out animals can also be used to screen drugs that may influence the biochemical, pathological, and behavioral parameters relevant to the particular physiological disorder being studied. Cell lines can also be derived from these animals for use as cellular models of the physiological disorder, or in drug screening.

Rational drug design

[0051] The goal of rational drug design is to produce structural analogs of biologically active polypeptides of interest or of small molecules with which they interact (e.g., agonists, antagonists, inhibitors) in order to fashion drugs which are, for example, more active or stable forms of the polypeptide, or which, e.g., enhance or interfere with the function of a polypeptide *in vivo*. Several approaches for use in rational drug design include analysis of three-dimensional structure, alanine scans, molecular modeling and use of anti-id antibodies. These techniques are well known to those skilled in the art. Such techniques may include providing atomic coordinates defining a three-dimensional structure of a protein complex formed by said first polypeptide and said second polypeptide, and designing or selecting compounds capable of interfering with the interaction between a first polypeptide and a second polypeptide based on said atomic coordinates.

[0052] Following identification of a substance which modulates or affects polypeptide activity, the substance may be further investigated. Furthermore, it may be manufactured and/or used in preparation, i.e., manufacture or formulation, or a composition such as a medicament, pharmaceutical composition or drug. These may be administered to individuals.

[0053] A substance identified as a modulator of polypeptide function may be peptide or non-peptide in nature. Non-peptide “small molecules” are often preferred for many *in vivo* pharmaceutical uses. Accordingly, a mimetic or mimic of the substance (particularly if a peptide) may be designed for pharmaceutical use.

[0054] The designing of mimetics to a known pharmaceutically active compound is a known approach to the development of pharmaceuticals based on a “lead” compound. This approach might be desirable where the active compound is difficult or expensive to synthesize or where it is unsuitable for a particular method of administration, e.g., pure peptides are unsuitable active agents for oral compositions as they tend to be quickly degraded by proteases in the alimentary canal. Mimetic design, synthesis and testing is generally used to avoid randomly screening large numbers of molecules for a target property.

[0055] Once the pharmacophore has been found, its structure is modeled according to its physical properties, e.g., stereochemistry, bonding, size and/or charge, using data from a range of sources, e.g., spectroscopic techniques, x-ray diffraction data and NMR. Computational analysis, similarity mapping (which models the charge and/or volume of a pharmacophore, rather than the bonding between atoms) and other techniques can be used in this modeling process.

[0056] A template molecule is then selected, onto which chemical groups that mimic the pharmacophore can be grafted. The template molecule and the chemical groups grafted thereon can be conveniently selected so that the mimetic is easy to synthesize, is likely to be pharmacologically acceptable, and does not degrade *in vivo*, while retaining the biological activity of the lead compound. Alternatively, where the mimetic is peptide-based, further stability can be achieved by cyclizing the peptide, increasing its rigidity. The mimetic or mimetics found by this approach can then be screened to see whether they have the target property, or to what extent it is exhibited. Further optimization or modification can then be carried out to arrive at one or more final mimetics for *in vivo* or clinical testing.

Diagnostic Assays

[0057] The identification of the interactions disclosed herein enables the development of diagnostic assays and kits, which can be used to determine a predisposition to or the existence of a physiological disorder. In one aspect, one of the proteins of the interaction is used to detect the presence of a “normal” second protein (i.e., normal with respect to its ability to interact with the first protein) in a cell extract or a biological fluid, and further, if desired, to detect the quantitative level of the second protein in the extract or biological fluid. The absence of the “normal” second protein would be indicative of a predisposition or existence of the physiological disorder. In a second aspect, an antibody against the protein complex is used to detect the presence and/or quantitative

level of the protein complex. The absence of the protein complex would be indicative of a predisposition or existence of the physiological disorder.

Nucleic Acids and Proteins

[0058] A nucleic acid or fragment thereof has substantial identity with another if, when optimally aligned (with appropriate nucleotide insertions or deletions) with the other nucleic acid (or its complementary strand), there is nucleotide sequence identity in at least about 60% of the nucleotide bases, usually at least about 70%, more usually at least about 80%, preferably at least about 90%, more preferably at least about 95% of the nucleotide bases, and more preferably at least about 98% of the nucleotide bases. A protein or fragment thereof has substantial identity with another if, optimally aligned, there is an amino acid sequence identity of at least about 30% identity with an entire naturally-occurring protein or a portion thereof, usually at least about 70% identity, more usually at least about 80% identity, preferably at least about 90% identity, more preferably at least about 95% identity, and most preferably at least about 98% identity.

[0059] Identity means the degree of sequence relatedness between two polypeptide or two polynucleotides sequences as determined by the identity of the match between two strings of such sequences. Identity can be readily calculated. While there exist a number of methods to measure identity between two polynucleotide or polypeptide sequences, the term "identity" is well known to skilled artisans (*Computational Molecular Biology*, Lesk, A. M., ed., Oxford University Press, New York, 1988; *Biocomputing: Informatics and Genome Projects*, Smith, D. W., ed., Academic Press, New York, 1993; *Computer Analysis of Sequence Data*, Part I, Griffin, A. M., and Griffin, H. G., eds., Humana Press, New Jersey, 1994; *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987; and *Sequence Analysis Primer*, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991). Methods commonly employed to determine identity between two sequences include, but are not limited to those disclosed in *Guide to Huge Computers*, Martin J. Bishop, ed., Academic Press, San Diego, 1994, and Carillo, H., and Lipman, D., *SIAM J Applied Math.* **48**:1073 (1988). Preferred methods to determine identity are designed to give the largest match between the two sequences tested. Such methods are codified in computer programs. Preferred computer program methods to determine identity between two sequences include, but are not limited to, GCG (Genetics Computer Group, Madison Wis.) program package (Devereux, J., et al., *Nucleic Acids Research* **12**(1).387 (1984)), BLASTP, BLASTN, FASTA (Altschul et al. (1990);

Altschul et al. (1997)). The well-known Smith Waterman algorithm may also be used to determine identity.

[0060] Alternatively, substantial homology or similarity exists when a nucleic acid or fragment thereof will hybridize to another nucleic acid (or a complementary strand thereof) under selective hybridization conditions, to a strand, or to its complement. Selectivity of hybridization exists when hybridization which is substantially more selective than total lack of specificity occurs. Nucleic acid hybridization will be affected by such conditions as salt concentration, temperature, or organic solvents, in addition to the base composition, length of the complementary strands, and the number of nucleotide base mismatches between the hybridizing nucleic acids, as will be readily appreciated by those skilled in the art. Stringent temperature conditions will generally include temperatures in excess of 30°C, typically in excess of 37°C, and preferably in excess of 45°C. Stringent salt conditions will ordinarily be less than 1000 mM, typically less than 500 mM, and preferably less than 200 mM. However, the combination of parameters is much more important than the measure of any single parameter. See, e.g., Asubel, 1992; Wetmur and Davidson, 1968.

[0061] The terms "isolated", "substantially pure", and "substantially homogeneous" are used interchangeably to describe a protein or polypeptide which has been separated from components which accompany it in its natural state. A monomeric protein is substantially pure when at least about 60 to 75% of a sample exhibits a single polypeptide sequence. A substantially pure protein will typically comprise about 60 to 90% W/W of a protein sample, more usually about 95%, and preferably will be over about 99% pure. Protein purity or homogeneity may be indicated by a number of means well known in the art, such as polyacrylamide gel electrophoresis of a protein sample, followed by visualizing a single polypeptide band upon staining the gel. For certain purposes, higher resolution may be provided by using HPLC or other means well known in the art which are utilized for purification.

[0062] Large amounts of the nucleic acids of the present invention may be produced by (a) replication in a suitable host or transgenic animals or (b) chemical synthesis using techniques well known in the art. Constructs prepared for introduction into a prokaryotic or eukaryotic host may comprise a replication system recognized by the host, including the intended polynucleotide fragment encoding the desired polypeptide, and will preferably also include transcription and translational initiation regulatory sequences operably linked to the polypeptide encoding segment. Expression vectors may include, for example, an origin of replication or autonomously replicating

sequence (ARS) and expression control sequences, a promoter, an enhancer and necessary processing information sites, such as ribosome-binding sites, RNA splice sites, polyadenylation sites, transcriptional terminator sequences, and mRNA stabilizing sequences. Secretion signals may also be included where appropriate which allow the protein to cross and/or lodge in cell membranes, and thus attain its functional topology, or be secreted from the cell. Such vectors may be prepared by means of standard recombinant techniques well known in the art.

[0063] The nucleic acid or protein may also be incorporated on a microarray. The preparation and use of microarrays are well known in the art. Generally, the microarray may contain the entire nucleic acid or protein, or it may contain one or more fragments of the nucleic acid or protein. Suitable nucleic acid fragments may include at least 17 nucleotides, at least 21 nucleotides, at least 30 nucleotides or at least 50 nucleotides of the nucleic acid sequence, particularly the coding sequence. Suitable protein fragments may include at least 4 amino acids, at least 8 amino acids, at least 12 amino acids, at least 15 amino acids, at least 17 amino acids or at least 20 amino acids. Thus, the present invention is also directed to such nucleic acid and protein fragments.

EXAMPLES

[0064] The present invention is further detailed in the following Examples, which are offered by way of illustration and are not intended to limit the invention in any manner. Standard techniques well known in the art or the techniques specifically described below are utilized.

EXAMPLE 1

Yeast Two-Hybrid System

[0065] The principles and methods of the yeast two-hybrid systems have been described in detail (Bartel and Fields, 1997). The following is thus a description of the particular procedure that we used, which was applied to all proteins.

[0066] The cDNA encoding the bait protein was generated by PCR from brain cDNA. Gene-specific primers were synthesized with appropriate tails added at their 5' ends to allow recombination into the vector pGBTQ. The tail for the forward primer was 5'-GCAGGAAACAGCTATGACCATACAGTCAGCGGCCGCCACC-3' (SEQ ID NO:1) and the tail for the reverse primer was 5'-ACGGCCAGTCGCGTGGAGTGTATGTCATGCGGCCGCTA-3' (SEQ ID NO:2). The tailed PCR product was then introduced by recombination into the yeast expression vector pGBTQ, which is a close derivative of pGBTC (Bartel et al., 1996) in which the polylinker site has been modified

to include M13 sequencing sites. The new construct was selected directly in the yeast J693 for its ability to drive tryptophane synthesis (genotype of this strain: Mat α , ade2, his3, leu2, trp1, URA3::GAL1-lacZ LYS2::GAL1-HIS3 gal4del gal80del cyhR2). In these yeast cells, the bait is produced as a C-terminal fusion protein with the DNA binding domain of the transcription factor Gal4 (amino acids 1 to 147). A total human brain (37 year-old male Caucasian) cDNA library cloned into the yeast expression vector pACT2 was purchased from Clontech (human brain MATCHMAKER cDNA, cat. # HL4004AH), transformed into the yeast strain J692 (genotype of this strain: Mat a, ade2, his3, leu2, trp1, URA3::GAL1-lacZ LYS2::GAL1-HIS3 gal4del gal80del cyhR2), and selected for the ability to drive leucine synthesis. In these yeast cells, each cDNA is expressed as a fusion protein with the transcription activation domain of the transcription factor Gal4 (amino acids 768 to 881) and a 9 amino acid hemagglutinin epitope tag. J693 cells (Mat α type) expressing the bait were then mated with J692 cells (Mat a type) expressing proteins from the brain library. The resulting diploid yeast cells expressing proteins interacting with the bait protein were selected for the ability to synthesize tryptophan, leucine, histidine, and β -galactosidase. DNA was prepared from each clone, transformed by electroporation into *E. coli* strain KC8 (Clontech KC8 electrocompetent cells, cat. # C2023-1), and the cells were selected on ampicillin-containing plates in the absence of either tryptophane (selection for the bait plasmid) or leucine (selection for the brain library plasmid). DNA for both plasmids was prepared and sequenced by di-deoxynucleotide chain termination method. The identity of the bait cDNA insert was confirmed and the cDNA insert from the brain library plasmid was identified using BLAST program against public nucleotides and protein databases. Plasmids from the brain library (preys) were then individually transformed into yeast cells together with a plasmid driving the synthesis of lamin fused to the Gal4 DNA binding domain. Clones that gave a positive signal after β -galactosidase assay were considered false-positives and discarded. Plasmids for the remaining clones were transformed into yeast cells together with plasmid for the original bait. Clones that gave a positive signal after β -galactosidase assay were considered true positives.

EXAMPLE 2

Identification of IKKb/LDHM Interaction

[0067] A yeast two-hybrid system as described in Example 1 using amino acids 301-602 of IKKb (GenBank (GB) accession no. AF031416) as bait was performed. One clone that was identified by this procedure included amino acids 9-332 of LDHM (GB accession no. U13679).

EXAMPLE 3

Identification of IKK-i/PN13730 Interaction

[0068] A yeast two-hybrid system as described in Example 1 using amino acids 450-717 of IKK-i (GenBank (GB) accession no. D63485) as bait was performed. One clone that was identified by this procedure included amino acids 203-493 of PN13730. The DNA sequence and the predicted protein sequence for PN13730 are set forth in Tables 13 and 14, respectively.

TABLE 13

Nucleotide Sequence of PN13730

gaaagtttcggttctgccccggcgggtggaccacgagcgcgtgccaccatggagctgaccactgctgagcagacagccaccgagggccgaaa
 ttctgagccttcctctggaccagcaggagacatacagacaagaaaggcgaactcaccatggcctccaccaatgcagagagccagctccaga
 gaatcatccgagacttgcaagatgctgtgacagaactaagcaagaatttcaggaagcaggggaacccatcacggatgacagcaccagcttgc
 ataaattttctataaacttgagtatctcctgcaatttgatcagaaagagaaggccaccctcctgggaacaagaaggactactgggattacttctgtg
 cctgcctggccaaggtgaaaggagccaatgatgggatccgctttgtcaagtctatctcagagctccgaacatccttggggaaaggaagagcattt
 attcgctactccttgggtgcaccagaggttggcagacaccttacagcagtgttcatgaacaccaaagtaccagtgactggtactatgcaagaagc
 ccctttctgcagccaaagctgagctcggacattgtgggccaactctatgagctgactgaggttcagtttgacctggcgtcaggggcttggacttgg
 atgctgcctggccaacatttgcaggaggacgtgaccactggctcttctgcttacctgtggaaacccctagccgcagctccagcatgagcagc
 ttggtgagcagctacctgcagactcaagagatgggtgtccactttgacctgaacagccccctaaacaacgaggcattggagggcttggatgagat
 gcgactagagctggaccagttggaggtgctgggagaagcagctacgggagcgcagcagctggacagagagaaccaggagctgagggg
 cagctgtcagccagcaaggggagcaactgcagacagagagggagagggggcgcaactgcagcggaggacaacgttcgctcacttgccttgggt
 agctgagctccagaagcagtgagggtgacccaggccaccagaacactgtgaaggagctgcagacatgcctgcagggcctggagctagga
 gcagcagagaaggaggaggactaccacacagccctgcggcggtggagtccatgctgcagccctggcacaggagcttggagccacacgg
 gactcactggacaagaaaaaccagcatttagccagcttcccagctggctagccatggctcagcagaaggcagatacggcatcagacacaaag
 ggccggcaagaacctattcccagtgatgcggcccaggagatgcaggagctaggggagaagcttcaagccctagaagggagagaaccaag
 gtcgaggagggtcaacagacagcagagtgtcccaactggaacagctgtgcaaggagcttgcagtgaaagaggatgcccgggccagcctggagc
 gcctggtgaaggagatggccccactccaggaggagttgtctgggaagggacaggaggcagaccagctctggcgacggctgcaggagttgct
 ggccccacacgagctcctgggaggaggagctagcagagttgaggggggagaaa (SEQ ID NO:3)

TABLE 14

Predicted Amino Acid Sequence of PN13730

MASTNAESQLQRIIRDLQDAVTELSKEFQEAGEPITDDSTSLHKFSYKLEYLLQFDQKEKAT
 LLGNKKDYWDYFCACLAQKVGANDGIRFVKISSELRTSLGKGRAFIRYSLVHQRLADTLQQ
 CFMNTKVTSDWYYARSPFLQPKLSSDIVGQLYELTEVQFDLASRGFDLDAAWPTFARRTL
 TGSSAYLWKPPSRSSSMSSLVSSYLQTQEMVSNFDLNSPLNNEALEGFDEMRLDQLEVR
 EKQLRERMQQLDRENQELRAAVSQQGEQLQTERERGRATAEDNVRLTCLVAELQKQWEV
 TQATQNTVKELQTCQLGLELGAEEKEEDYHTALRRLESMLQPLAQELEATRSLDKKNQH
 LASFPGWLAMAQQKADTASDTKGRQEPIPSDAAQEMQELGEKLQALERERTKVEEVNRQQ
 SAQLEQLVKELQLKEDARASLERLVKEMAPLQEELSGKGQEADQLWRRLLQELLAHTSSWE
 EELAE LRREK (SEQ ID NO:4)

EXAMPLES 4-13

Identification of Protein-Protein Interactions

[0069] A yeast two-hybrid system as described in Example 1 using amino acids of the bait as set forth in Table 15 was performed. The clone that was identified by this procedure for each bait is set forth in Table 15 as the prey. The “AA” refers to the amino acids of the bait or prey. The “NUC” refers to the nucleotides of the bait or prey. The Accession numbers refer to GB: GenBank accession numbers.

TABLE 15

Ex.	BAIT	ACCESSION	COORDINATES	PREY	ACCESSION	COORDINATES
4	IKKb	GB: AF031416	AA: 301-602	EIF3S10	GB: D50929	AA 666-852
5	IKKb	GB: AF031416	AA 301-602	SLAP2	GB: AF100750	AA 16-258
6	IKKb	GB: AF031416	AA 301-602	KIAA0614	GB: AB014514	AA 549-874
7	IKKb	GB: AF031416	AA 301-602	SART-1	GB: AB006198	AA 248-419
8	IKKb	GB: AF031416	AA 301-602	GBDR1	GB: NM_006318	AA 4-114
9	IKKa	GB: AF009225	AA 599-638	GBDR1	GB: NM_006318	AA 4-114
10	IKKg	GB: AF074382	AA 150-302	I-TRAF	GB: U59683	AA 17-424
11	IKK-i	GB: D63485	AA 450-717	I-TRAF	GB: U59683	AA 17-424
12	IKK-i	GB: D63485	AA 450-717	NUMA1	GB: Z11583	AA 962-1092
13	IKK-i	GB: D63485	AA 450-717	SPA-1	GB: AB005666	AA 925-1042

EXAMPLE 14

Generation of Polyclonal Antibody Against Protein Complexes

[0070] As shown above, IKKb interacts with LDHM to form a complex. A complex of the two proteins is prepared, e.g., by mixing purified preparations of each of the two proteins. If
 5 desired, the protein complex can be stabilized by cross-linking the proteins in the complex, by methods known to those of skill in the art. The protein complex is used to immunize rabbits and mice using a procedure similar to that described by Harlow et al. (1988). This procedure has been shown to generate Abs against various other proteins (for example, see Kraemer et al., 1993).

[0071] Briefly, purified protein complex is used as immunogen in rabbits. Rabbits are immunized with 100 µg of the protein in complete Freund's adjuvant and boosted twice in three-week intervals, first with 100 µg of immunogen in incomplete Freund's adjuvant, and followed by 100 µg of immunogen in PBS. Antibody-containing serum is collected two weeks thereafter. The antisera is preadsorbed with IKKb and LDHM, such that the remaining antisera comprises antibodies which bind conformational epitopes, i.e., complex-specific epitopes, present on the IKKb-LDHM complex but not on the monomers.

[0072] Polyclonal antibodies against each of the complexes set forth in Tables 1-12 are prepared in a similar manner by mixing the specified proteins together, immunizing an animal and isolating antibodies specific for the protein complex, but not for the individual proteins.

[0073] Polyclonal antibodies against the protein set forth in Table 14 are prepared in a
 20 similar manner by immunizing an animal with the protein and isolating antibodies specific for the protein.

EXAMPLE 15

Generation of Monoclonal Antibodies Specific for Protein Complexes

[0074] Monoclonal antibodies are generated according to the following protocol. Mice are immunized with immunogen comprising IKKb/LDHM complexes conjugated to keyhole limpet hemocyanin using glutaraldehyde or EDC as is well known in the art. The complexes can be prepared as described in Example 14, and may also be stabilized by cross-linking. The immunogen is mixed with an adjuvant. Each mouse receives four injections of 10 to 100 µg of immunogen, and
 30 after the fourth injection blood samples are taken from the mice to determine if the serum contains antibody to the immunogen. Serum titer is determined by ELISA or RIA. Mice with sera indicating the presence of antibody to the immunogen are selected for hybridoma production.

[0075] Spleens are removed from immune mice and a single-cell suspension is prepared (Harlow et al., 1988). Cell fusions are performed essentially as described by Kohler et al. (1975). Briefly, P3.65.3 myeloma cells (American Type Culture Collection, Rockville, MD) or NS-1 myeloma cells are fused with immune spleen cells using polyethylene glycol as described by Harlow et al. (1988). Cells are plated at a density of 2×10^5 cells/well in 96-well tissue culture plates. Individual wells are examined for growth, and the supernatants of wells with growth are tested for the presence of IKKb/LDHM complex-specific antibodies by ELISA or RIA using IKKb/LDHM complex as target protein. Cells in positive wells are expanded and subcloned to establish and confirm monoclonality.

[0076] Clones with the desired specificities are expanded and grown as ascites in mice or in a hollow fiber system to produce sufficient quantities of antibodies for characterization and assay development. Antibodies are tested for binding to IKKb alone or to LDHM alone, to determine which are specific for the IKKb/LDHM complex as opposed to those that bind to the individual proteins.

[0077] Monoclonal antibodies against each of the complexes set forth in Tables 1-12 are prepared in a similar manner by mixing the specified proteins together, immunizing an animal, fusing spleen cells with myeloma cells and isolating clones which produce antibodies specific for the protein complex, but not for the individual proteins.

[0078] Monoclonal antibodies against the protein set forth in Table 14 are prepared in a similar manner by immunizing an animal with the protein, fusing spleen cells with myeloma cells and isolating clones which produce antibodies specific for the protein.

EXAMPLE 16

In vitro Identification of Modulators for Protein-Protein Interactions

[0079] The present invention is useful in screening for agents that modulate the interaction of IKKb and LDHM. The knowledge that IKKb and LDHM form a complex is useful in designing such assays. Candidate agents are screened by mixing IKKb and LDHM (a) in the presence of a candidate agent, and (b) in the absence of the candidate agent. The amount of complex formed is measured for each sample. An agent modulates the interaction of IKKb and LDHM if the amount of complex formed in the presence of the agent is greater than (promoting the interaction), or less than (inhibiting the interaction) the amount of complex formed in the absence of the agent. The

amount of complex is measured by a binding assay, which shows the formation of the complex, or by using antibodies immunoreactive to the complex.

[0080] Briefly, a binding assay is performed in which immobilized IKKb is used to bind labeled LDHM. The labeled LDHM is contacted with the immobilized IKKb under aqueous conditions that permit specific binding of the two proteins to form a IKKb/LDHM complex in the absence of an added test agent. Particular aqueous conditions may be selected according to conventional methods. Any reaction condition can be used as long as specific binding of IKKb/LDHM occurs in the control reaction. A parallel binding assay is performed in which the test agent is added to the reaction mixture. The amount of labeled LDHM bound to the immobilized IKKb is determined for the reactions in the absence or presence of the test agent. If the amount of bound, labeled LDHM in the presence of the test agent is different than the amount of bound labeled LDHM in the absence of the test agent, the test agent is a modulator of the interaction of IKKb and LDHM.

[0081] Candidate agents for modulating the interaction of each of the protein complexes set forth in Tables 1-12 are screened *in vitro* in a similar manner.

EXAMPLE 17

In vivo Identification of Modulators for Protein-Protein Interactions

[0082] In addition to the *in vitro* method described in Example 16, an *in vivo* assay can also be used to screen for agents which modulate the interaction of IKKb and LDHM. Briefly, a yeast two-hybrid system is used in which the yeast cells express (1) a first fusion protein comprising IKKb or a fragment thereof and a first transcriptional regulatory protein sequence, e.g., GAL4 activation domain, (2) a second fusion protein comprising LDHM or a fragment thereof and a second transcriptional regulatory protein sequence, e.g., GAL4 DNA-binding domain, and (3) a reporter gene, e.g., β -galactosidase, which is transcribed when an intermolecular complex comprising the first fusion protein and the second fusion protein is formed. Parallel reactions are performed in the absence of a test agent as the control and in the presence of the test agent. A functional IKKb/LDHM complex is detected by detecting the amount of reporter gene expressed. If the amount of reporter gene expression in the presence of the test agent is different than the amount of reporter gene expression in the absence of the test agent, the test agent is a modulator of the interaction of IKKb and LDHM.

[0083] Candidate agents for modulating the interaction of each of the protein complexes set forth in Tables 1-12 are screened *in vivo* in a similar manner.

[0084] While the invention has been disclosed in this patent application by reference to the details of preferred embodiments of the invention, it is to be understood that the disclosure is intended in an illustrative rather than in a limiting sense, as it is contemplated that modifications will readily occur to those skilled in the art, within the spirit of the invention and the scope of the appended claims.

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PCT Published Application No. WO 97/27296

PCT Published Application No. WO 99/65939

U.S. Patent No. 5,622,852

U.S. Patent No. 5,773,218

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